RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 09/526, 298 _____

Source: _____ JFW16, _____

Date Processed by STIC: _____ 05/30/2006 _____

ENTERED

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

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1                               SEQUENCE LISTING
2
3    (1)      General Information:
4
5         (i) APPLICANT: EVANS, RONALD M.
6                        MCKEOWN, MICHAEL B.
7                        ORO, ANTHONY E.
8                        SEGRAVES, WILLIAM A.
9                        YAO, TSO-PANG
10
11      (ii) TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE
12               STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE
13               ULTRASPIRACLE RECEPTOR
14
15     (iii) NUMBER OF SEQUENCES: 29
16
17      (iv) CORRESPONDENCE ADDRESS:
18               (A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
19               (B) STREET: 444 South Flower Street, Suite 2000
20               (C) CITY: Los Angeles
21               (D) STATE: California
22               (E) COUNTRY: United States
23               (F) ZIP: 90071
24
25       (v) COMPUTER READABLE FORM:
26               (A) MEDIUM TYPE: Floppy disk
27               (B) COMPUTER: IBM PC compatible
28               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
30
31      (vi) CURRENT APPLICATION DATA:
32               (A) APPLICATION NUMBER: US 09/526,298
33               (B) FILING DATE: 15-MARCH-2000
34               (C) CLASSIFICATION:
35     (vii) PRIOR APPLICATION DATA:
36               (A) APPLICATION NUMBER: US 07/907,908
37               (B) FILING DATE: 02-JUL-1992
38               (C) CLASSIFICATION:
39    (viii) ATTORNEY/AGENT INFORMATION:
40               (A) NAME: Reiter,, Stephen E.
41               (B) REGISTRATION NUMBER: 31192
42               (C) REFERENCE/DOCKET NUMBER: P41 9321
43
44      (ix) TELECOMMUNICATION INFORMATION:
45               (A) TELEPHONE: (619) 546-4737
46               (B) TELEFAX: (619) 546-9392
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47
48
49      (2) INFORMATION FOR SEQ ID NO:1:
50
51          (i) SEQUENCE CHARACTERISTICS:
52                  (A) LENGTH: 2304 base pairs
53                  (B) TYPE: nucleic acid
54                  (C) STRANDEDNESS: single
55                  (D) TOPOLOGY: linear
56
57          (ii) MOLECULE TYPE: DNA (genomic)
58
59
60          (ix) FEATURE:
61                  (A) NAME/KEY: CDS
62                  (B) LOCATION: 163..1701
63
64
65          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67      GGACACGGTG GCGTTGGCAA AGTGAAACCC CAACAGAGAG GCGAAAGCGA GCCAAGACAC          60
68
69      ACCACATACA CACGAAGAGA ACGAGCAAGA AGAAACCGGT AGGCGGAGGA GGCGCTGCCC         120
70
71      CCAGTTCCTC CAATATACCC AGCACCACAT CACAAGCCCA GG ATG GAC AAC TGC           174
72                                                     Met Asp Asn Cys
73                                                      1
74
75      GAC CAG GAC GCC AGC TTT CGG CTG AGC CAC ATC AAG GAG GAG GTC AAG         222
76      Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys Glu Glu Val Lys
77       5                  10                  15                  20
78
79      CCG GAC ATC TCG CAG CTG AAC GAC AGC AAC AAC AGC AGC TTT TCG CCC         270
80      Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser Ser Phe Ser Pro
81                      25                  30                  35
82
83      AAG GCC GAG AGT CCC GTG CCC TTC ATG CAG GCC ATG TCC ATG GTC CAC         318
84      Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met Ser Met Val His
85                      40                  45                  50
86
87      GTG CTG CCC GGC TCC AAC TCC GCC AGC TCC AAC AAC AAC AGC GCT GGA         366
88      Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn Asn Ser Ala Gly
89                      55                  60                  65
90
91      GAT GCC CAA ATG GCG CAG GCG CCC AAT TCG GCT GGA GGC TCT GCC GCC         414
92      Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly Gly Ser Ala Ala
93           70                  75                  80
94
95      GCT GCA GTC CAG CAG CAG TAT CCG CCT AAC CAT CCG CTG AGC GGC AGC         462
96      Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro Leu Ser Gly Ser
97       85                  90                  95                 100
98
99      AAG CAC CTC TGC TCT ATT TGC GGG GAT CGG GCC AGT GGC AAG CAC TAC         510
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100    Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr
101                    105              110              115
102
103    GGC GTG TAC AGC TGT GAG GGC TGC AAG GGC TTC TTT AAA CGC ACA GTG        558
104    Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val
105                    120              125              130
106
107    CGC AAG GAT CTC ACA TAC GCT TGC AGG GAG AAC CGC AAC TGC ATC ATA        606
108    Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg Asn Cys Ile Ile
109            135              140              145
110
111    GAC AAG CGG CAG AGG AAC CGC TGC CAG TAC TGC CGC TAC CAG AAG TGC        654
112    Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys
113        150              155              160
114
115    CTA ACC TGC GGC ATG AAG CGC GAA GCG GTC CAG GAG GAG CGT CAA CGC        702
116    Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg
117    165              170              175              180
118
119    GGC GCC CGC AAT GCG GCG GGT AGG CTC AGC GCC AGC GGA GGC GGC AGT        750
120    Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser Gly Gly Gly Ser
121                    185              190              195
122
123    AGC GGT CCA GGT TCG GTA GGC GGA TCC AGC TCT CAA GGC GGA GGA GGA        798
124    Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln Gly Gly Gly Gly
125                    200              205              210
126
127    GGA GGC GGC GTT TCT GGC GGA ATG GGC AGC GGC AAC GGT TCT GAT GAC        846
128    Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn Gly Ser Asp Asp
129            215              220              225
130
131    TTC ATG ACC AAT AGC GTG TCC AGG GAT TTC TCG ATC GAG CGC ATC ATA        894
132    Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile Glu Arg Ile Ile
133        230              235              240
134
135    GAG GCC GAG CAG CGA GCG GAG ACC CAA TGC GGC GAT CGT GCA CTG ACG        942
136    Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp Arg Ala Leu Thr
137    245              250              255              260
138
139    TTC CTG CGC GTT GGT CCC TAT TCC ACA GTC CAG CCG GAC TAC AAG GGT        990
140    Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro Asp Tyr Lys Gly
141                    265              270              275
142
143    GCC GTG TCG GCC CTG TGC CAA GTG GTC AAC AAA CAG CTC TTC CAG ATG       1038
144    Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln Leu Phe Gln Met
145                    280              285              290
146
147    GTC GAA TAC GCG CGC ATG ATG CCG CAC TTT GCC CAG GTG CCG CTG GAC       1086
148    Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln Val Pro Leu Asp
149            295              300              305
150
151    GAC CAG GTG ATT CTG CTG AAA GCC GCT TGG ATC GAG CTG CTC ATT GCG       1134
152    Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu Leu Leu Ile Ala
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INPUT SET: S30829.raw

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153        310                  315                  320
154
155   AAC GTG GCC TGG TGC AGC ATC GTT TCG CTG GAT GAC GGC GGT GCC GGC     1182
156   Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp Gly Gly Ala Gly
157   325                  330                  335                  340
158
159   GGC GGG GGC GGT GGA CTA GGC CAC GAT GGC TCC TTT GAG CGA CGA TCA     1230
160   Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe Glu Arg Arg Ser
161                  345                  350                  355
162
163   CCG GGC CTT CAG CCC CAG CAG CTG TTC CTC AAC CAG AGC TTC TCG TAC     1278
164   Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln Ser Phe Ser Tyr
165                  360                  365                  370
166
167   CAT CGC AAC AGT GCG ATC AAA GCC GGT GTG TCA GCC ATC TTC GAC CGC     1326
168   His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala Ile Phe Asp Arg
169                  375                  380                  385
170
171   ATA TTG TCG GAG CTG AGT GTA AAG ATG AAG CGG CTG AAT CTC GAC CGA     1374
172   Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu Asn Leu Asp Arg
173        390                  395                  400       .
174
175   CGC GAG CTG TCC TGC TTG AAG GCC ATC ATA CTG TAC AAC CCG GAC ATA     1422
176   Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr Asn Pro Asp Ile
177   405                  410                  415                  420
178
179   CGC GGG ATC AAG AGC CGG GCG GAG ATC GAG ATG TGC CGC GAG AAG GTG     1470
180   Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys Arg Glu Lys Val
181                  425                  430                  435
182
183   TAC GCT TGC CTG GAC GAG CAC TGC CGC CTG GAA CAT CCG GGC GAC GAT     1518
184   Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His Pro Gly Asp Asp
185                  440                  445                  450   .
186
187   GGA CGC TTT GCG CAA CTG CTG CTG CGT CTG CGC CGC TTT GCG ATC GAT     1566
188   Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Arg Arg Phe Ala Ile Asp
189        455                  460                  465
190
191   CAG CCT GAA GTG CCA GGA TCA CCT GTT CCT CTT CCG CAT TAC CAG CGA     1614
192   Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro His Tyr Gln Arg
193        470                  475                  480
194
195   CCG GCC GCT GGA GGA GCT CTT TCT CGA GCA GCT GGA GGC GCC GCC GCC     1662
196   Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly Gly Ala Ala Ala
197   485                  490                  495                  500
198
199   ACC CGG CCT GGC GAT GAA ACT GGA GTA GGG TCC CGA CTC TAAAGTCGCC     1711
200   Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg Leu
201                  505                  510
202
203   CCCGTTCTCC ATCCGAAAAA TGTTTCATTG TGATTGCGTT TGTTTGCATT TCTCCTCTCT     1771
204
205   ATCCCTACAA AAGCCCCCTA ATATTACGCA AAATGTGTAT GTAATTGTTT ATTTTTTTTT     1831
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INPUT SET: S30829.raw

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206
207    TATTACCTAA TATTATTATT ATTATTGATA TAGAAAATGT TTTCCTTAAG ATGAAGATTA    1891
208
209    GCCTCCTCGA CGTTTATGTC CCAGTAAACG AAAAACAAAC AAAATCCAAA ACTTGAAAAG    1951
210
211    AACACAAAAC ACGAACGAGA AAATGCACAC AAGCAAAGTA AAAGTAAAAG TTAAACTAAA    2011
212
213    GCTAAACGAG TAAAGATATT AAAATAACGG TTAAAATTAA TGCATAGTTA TGATCTACAG    2071
214
215    ACGTATGTAA ACATACAAAT TCAGCATAAA TATATATGTC AGCAGGCGCA TATCTGCGGT    2131
216
217    GCTGGCCCCG TTCTAAACCA ATTGTAATTA CTTTTTAACA TAAATTTACC CAAAACGTTA    2191
218
219    TCAATTAGAT GCGAGATACA AAAATCACCG ACGAAAACCA ACAAAATATA TCTATGTATA    2251
220
221    AAAAATATAA GCTGCATAAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA           2304
222
223
224    (2) INFORMATION FOR SEQ ID NO:2:
225
226          (i) SEQUENCE CHARACTERISTICS:
227                (A) LENGTH: 513 amino acids
228                (B) TYPE: amino acid
229                (D) TOPOLOGY: linear
230
231          (ii) MOLECULE TYPE: protein
232
233          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
234
235    Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys
236     1               5                  10                  15
237
238    Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser
239                20                  25                  30
240
241    Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met
242            35                  40                  45
243
244    Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn
245        50                  55                  60
246
247    Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly
248     65                  70                  75                  80
249
250    Gly Ser Ala Ala Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro
251                85                  90                  95
252
253    Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser
254            100                 105                 110
255
256    Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe
257            115                 120                 125
258
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